AMENDMENTS TO THE CLAIMS

1. (original) A mass spectroscopy system comprising:

ionization means for ionizing a substance as an object of measurement for a mass spectrometer; and

means for selecting an ion species with a specific mass-to-charge ratio m/z from ions produced by said ionization means and dissociating the same, wherein the selection, dissociation and measurement of the ion species as the measurement object are repeated in a plurality of stages, said mass spectroscopy system further comprising:

mass spectroscopy data acquisition means for performing the selection and dissociation of an ion species n-1 times (n ≥ 1, where n is an integer) and acquiring a peak of measurement intensity against the mass-to-charge ratio of the ion that has been selected and dissociated;

correspondence determination means for comparing the peak of measurement intensity against the mass-to-charge ratio of the ion that is obtained by the mass spectroscopy data acquisition means with the characteristics data of a certain ion species in order to determine the possibility of correspondence of the ion that has been selected and dissociated to the certain ion species; and

next-analysis content determination means for determining the analysis content in an n-th stage mass spectroscopy based on the result of determination by said correspondence determination means.

2. (original) The mass spectroscopy system according to claim 1, wherein an ion peak corresponding to an ion that has been determined to correspond to the predetermined ion species is avoided from being selected as the target for the selection and dissociation in the next analysis.

3. (original) The mass spectroscopy system according to claim 1, wherein in the next analysis content in the n-th stage mass spectroscopy determined by said next analysis content determination means, an ion species with a certain m/z value is selected from the n-th stage mass spectrum, an n-th dissociation is conducted, and an n+1-th stage mass spectroscopy measurement is conducted.

4. (original) The mass spectroscopy system according to claim 1, wherein in the next analysis content in the n-th stage mass spectroscopy determined by the next analysis content determination means, an ion peak is selected from the n-1-th stage mass spectrum measurement result that has a different m/z value from that of the ion peak with the certain m/z value that has been selected in the n-1-th stage mass spectrum when the n-th stage mass spectrum measurement result was obtained, the thus selected ion peak is dissociated, and the n-th stage mass spectroscopy is repeated.

5. (original) The mass spectroscopy system according to claim 1, wherein said correspondence determination means determines correspondence within a certain tolerance or range.

6. (original) A mass spectroscopy system comprising:

ionization means for ionizing a substance as an object of measurement for a mass spectrometer; and

mass spectroscopy means for selecting an ion species with a specific mass-to-charge ratio m/z from ions produced by said ionization means and dissociating the same, and for repeating the selection, dissociation and measurement of the ion species as the

3

measurement object in a plurality of stages, said mass spectroscopy system further comprising:

mass spectroscopy data acquisition means for acquiring information about a peak of measurement intensity against the mass-to-charge ratio of an n-th stage ion obtained by said mass spectroscopy means;

isotope peak determination means for determining an isotope peak based on ion mass spectroscopy data acquired by said mass spectroscopy data acquisition means; and

next analysis content determination means for determining the next n-th stage analysis content based on the isotope peak determined by said isotope peak determination means.

7. (original) A mass spectroscopy system according to claim 1, wherein, in the case where there is a mixture of a sample that is labeled by an isotope and a sample that is not labeled by an isotope in a preprocessing stage of mass spectroscopy, the characteristics data of the predetermined ion species is the characteristics data of an ion derived from the sample labeled by an isotope.

8. (original) A mass spectroscopy system comprising:

an ion source for ionizing a sample;

a mass spectroscopy portion for performing a primary mass spectroscopy on an ion obtained by ionizing said sample and performing a secondary mass spectroscopy, following said primary mass spectroscopy, on a dissociated ion produced by dissociating said ion;

an RF power supply for applying an RF voltage for eliminating ions that are not analysis objects prior to said primary mass spectroscopy; and

a control portion for outputting a instruction for the elimination of the non-analysis object ions to said RF power supply.

9. (original) The mass spectroscopy system according to claim 8, wherein said control portion further comprises means for selecting an analysis object ion as the object of said secondary mass spectroscopy following said primary mass spectroscopy.

10. (original) The mass spectroscopy system according to claim 8, further comprising a display portion for allowing the designation of said analysis object ion and said non-analysis object ions.

11. (original) The mass spectroscopy system according to claim 8, comprising a trap portion for trapping said ion, wherein an RF voltage is applied from said RF power supply to said trap portion in order to eliminate said non-analysis ions prior to said primary mass spectroscopy.

12. (original) The mass spectroscopy system according to claim 8, further comprising a selection portion for selecting a data sequence of a substance as an analysis object candidate substance, and a first database for searching for the data sequence of said analysis object candidate substance, wherein said control portion outputs an instruction for performing mass spectroscopy on a dissociated ion produced by dissociating a substance retrieved concerning the data sequence of said analysis object candidate substance, and wherein said mass spectroscopy portion conducts mass spectroscopy on an ion derived from the retrieved substance in response to the instruction from said control portion.

5

13. (original) The mass spectroscopy system according to claim 12, wherein said first database communicates with an external database so that a file concerning the data sequence of said analysis object candidate substance can be updated.

14. (original) A mass spectrum measurement employing an apparatus comprising an ion source, a mass spectroscopy portion, and an RF power supply, said method comprising:

ionizing a sample using said ion source;

selectively eliminating non-analysis object ions from the ions obtained by the ionization, using said RF power supply;

performing a primary mass spectroscopy on said ion in said mass spectroscopy portion, following the elimination step; and

performing a secondary mass spectroscopy on a dissociated ion produced by dissociating said ion following said primary mass spectroscopy.

15. (original) The mass spectrum measurement according to claim 14, wherein, in said mass spectroscopy portion, an analysis object ion as the object of said secondary mass spectroscopy is selectively dissociated, following said primary mass spectroscopy, and a resultant dissociated ion is subjected to secondary mass spectroscopy.

16. (original) The mass spectrum measurement according to claim 14, wherein, using said apparatus further comprising a first database in which a data sequence of an analysis object candidate substance is recorded and a control portion, from the data concerning said primary mass spectroscopy that is entered from said mass spectroscopy portion, data that corresponds to the data contained in said first database is retrieved, and

6

an ion concerning the corresponding data is selectively dissociated, and a resultant dissociated ion is subjected to said secondary mass spectroscopy in said mass spectroscopy portion.

17. (original) The mass spectrum measurement according to claim 16, wherein, in said first database, the data about said analysis object candidate substance is stored in terms of a data structure for each of the species including the human species and other species.

18. (original) The mass spectrum measurement according to claim 16, wherein said RF power supply applies an RF voltage in order to eliminate an ion that does not correspond to the data in said first database prior to said primary mass spectroscopy, and wherein said control portion outputs instructions for the elimination of said ion that does not correspond, said dissociation after said primary mass spectroscopy, and the carrying out of said secondary mass spectroscopy.

19. (original) The mass spectrum measurement according to claim 18, wherein in said first database, the data about an analysis object candidate substance is stored in terms of a data structure for each of the species including the human species and other species.

20. (original) The mass spectrum measurement according to claim 16, wherein, using said apparatus that further comprises a second database in which data about non-analysis object candidate substance is recorded, a non-analysis object ion that corresponds to the data contained in said secondary database is eliminated prior to primary

7

mass spectroscopy so that an analysis object ion can be selectively subjected to said primary mass spectroscopy.

21. (original) The mass spectrum measurement according to claim 20, wherein said RF power supply applies an RF voltage in order to eliminate a non-analysis object ion that corresponds to the data in said second database prior to said primary mass spectroscopy, and wherein said control portion outputs instructions for the elimination of said non-analysis object ion, the dissociation of said analysis object ion following said primary mass spectroscopy, and the carrying out of said secondary mass spectroscopy.

22. (original) The mass spectrum measurement according to claim 21, wherein an internal standard substance is added to a sample comprising said ion, and the analysis object substance is quantitatively determined.

23. (original) A mass spectroscopy apparatus comprising:

an ion source for ionizing a sample;

a first database in which a data sequence of an analysis object candidate substance is recorded;

a control portion for issuing an instruction for selecting an analysis object ion that corresponds to the data in said first database; and

a mass spectroscopy portion for performing a primary mass spectroscopy on an ion obtained by ionizing said sample and subjecting a dissociated ion produced by the dissociation of the selected analysis object ion to a secondary mass spectroscopy.

24. (original) The mass spectroscopy apparatus according to claim 23, further comprising an RF power supply, wherein said RF power supply applies an RF voltage in order to eliminate an ion that does not correspond to the data in said first database prior to said primary mass spectroscopy, and wherein said control portion comprises means for carrying out the elimination of the ion that does not correspond, the dissociation of said analysis object ion following said primary mass spectroscopy, and said secondary mass spectroscopy.

25. (original) The mass spectroscopy apparatus according to claim 24, further comprising an RF power supply, wherein said RF power supply applies an RF voltage in order to eliminate a non-analysis object ion that corresponds to the data in said second database prior to said primary mass spectroscopy, and wherein said control portion comprises means for carrying out the elimination of said non-analysis object ion, the dissociation of said analysis object ion following said primary mass spectroscopy, and said secondary mass spectroscopy.

26. (new) A mass spectroscopy system according to claim 1, wherein said characteristics data include the mass number, valence, mass-to-charge ratio m/z value, and detection intensity of an ion species, the retention time of liquid chromatography (LC) or gas chromatography (GC), the solvent for LC or GC or its mobile-phase ratio, the flow volume or gradient of LC or GC, a sample number of the sample that has been divided during the ion exchange in the one-dimensional LC in cases where a two-dimensional LC is used, the spot position, number or coordinates on a sample plate in cases where a MALDI ion source is employed, the content of measures to be taken for each of the ion species that corresponded to the stored characteristics data, analysis conditions including the date/time of measurement, a column number of the LC or GC used, an order n of the tandem mass spectroscopy MS^n, and the operating condition of the mass spectrometer, and information about the inferred structure of an ion species.

27. (new) The mass spectroscopy system according to claim 26, wherein the content of measures to be taken is in accordance with a user specification.

28. (new) The mass spectroscopy system according to claim 26, wherein the user specification includes at least one of whether or not a particular ion species should be excluded from the target ion species for the next MS^n ($n \geq 1$) analysis, whether or not a particular ion species should be selected as the target ion species for the next MS^n ($n \geq 1$) analysis, and whether or not the particular ion species should be removed upon or prior to the injection of an ion sample into the mass spectroscopy system.

29. (new) The mass spectroscopy system according to claim 26, wherein the ion species is an amino acid sequence, as in cases involving a protein or peptide sample.

30. (new) The mass spectroscopy system according to claim 26, further comprising a function for automatically correcting or calibrating the retention time of actually measured data concerning liquid chromatography (LC) or gas chromatography (GC) on the basis of a comparison between an actually measured retention time of a designated reference substance and a retention time of a reference substance that is already stored in a database provided in the system.

31. (new) The mass spectroscopy system according to claim 26, further comprising a function whereby:

the mass number of an ion species is automatically corrected or calibrated to be the mass number without isotopes if the ion species is accompanied by an isotope peak upon deriving of the mass number, and whereby;

10

the mass-to-charge ratio m/z value of the ion species is automatically corrected or calibrated if the m/z value fluctuates as time elapses from the start of measurement, on the basis of a comparison between an actually measured m/z value of at least one reference substance with a known m/z value that is contained in the sample, and the known m/z value, wherein said actually measured m/z value is those of the reference substances with different retention times of LC or GC in the case where there is more than one reference substance.